



## NOAA SCIENTIFIC PUBLICATIONS REPORT

### JUNE 19, 2015

#### **HIGHLIGHTED ARTICLES**

[Adrenal gland and lung lesions in Gulf of Mexico common bottlenose dolphins \(\*Tursiops truncatus\*\) found dead following the Deepwater Horizon oil spill](#)

PLoS ONE (3.534)

[Seasonal variation in the skin transcriptome of common bottlenose dolphins \(\*Tursiops truncatus\*\) from the northern Gulf of Mexico](#)

PLoS ONE (3.534)

[Photogrammetry of killer whales using a small hexacopter launched at sea](#)

Journal of Unmanned Vehicle Systems

[Spatial and temporal changes in cumulative human impacts on the world's ocean](#)

Nature Communications (10.742)

#### **ADDITIONAL ARTICLES**

##### **NWS Publications**

[Ensemble Bayesian forecasting system Part I: Theory and algorithms](#)

Journal of Hydrology (2.693)

[Hydroclimatic Conditions Preceding the March 2014 Oso Landslide](#)

Journal of Hydrometeorology (3.57)

##### **NESDIS Publications**

[Data stewardship: How NOAA delivers environmental information for today and tomorrow](#)

Marine Technology Society Journal (0.76)

[A metadata template for ocean acidification data](#)

Earth System Science Data (ALM: 176 downloads since 11 June 2015)



## NOAA SCIENTIFIC PUBLICATIONS REPORT

### JUNE 19, 2015

#### NMFS Publications

[Mixed stock analysis of a resident green turtle, \*Chelonia mydas\*, population in New Caledonia links rookeries in the South Pacific](#)

Wildlife Research (1.194)

[Variation in phytoplankton composition between two North Pacific frontal zones along 158°W during winter-spring 2008-2011](#)

Progress in Oceanography (3.986)

[Using a remotely operated vehicle \(ROV\) to observe loggerhead sea turtle \(\*Caretta caretta\*\) behavior on foraging grounds off the mid-Atlantic United States](#)

Journal of Experimental Marine Biology and Ecology (2.475)

[Stable isotope models predict foraging habitat of Northern Fur Seals \(\*Callorhinus ursinus\*\) in Alaska](#)

PLoS ONE (3.534)

[The ability of blue crab \(\*Callinectes sapidus\*, Rathbun 1886\) to sustain aerobic metabolism during hypoxia](#)

Journal of Experimental Marine Biology and Ecology (2.475)

[Stock composition and ocean spatial distribution inference from California recreational Chinook salmon fisheries using Genetic Stock Identification](#)

Fisheries Research (1.843)

[Geostatistical delta-generalized linear mixed models improve precision for estimated abundance indices for West Coast groundfishes](#)

ICES Journal of Marine Science (2.525)

[A comparison of single and multiple stressor protocols to assess acute stress in a coastal shark species, \*Rhizoprionodon terraenovae\*](#)



## NOAA SCIENTIFIC PUBLICATIONS REPORT

### JUNE 19, 2015

Fish Physiology and Biochemistry (1.68)

[Age at maturity, skipped spawning, fecundity, and site fidelity of female sablefish \(\*Anoplopoma fimbria\*\) during the spawning season](#)

Fishery Bulletin (1.783)

[Mixed effects: a unifying framework for statistical modelling in fisheries biology](#)

ICES Journal of Marine Science (2.525)

[Genetic origins of immature green turtles \(\*Chelonia mydas\*\) at two foraging grounds in Sabah, Malaysia](#)

Endangered Species Research (2.259)

[Productivity change and fleet restructuring after transition to individual transferable quota management](#)

Marine Policy (2.621)

Joint Line Office Publications

[Synthesis of Arctic Research \(SOAR\) in marine ecosystems of the Pacific Arctic](#)

Progress in Oceanography (3.986)

[NOAA's role in defining the U.S. Extended Continental Shelf](#)

Marine Technology Society Journal (0.687)

### **HIGHLIGHTED ARTICLES**

*Adrenal gland and lung lesions in Gulf of Mexico common bottlenose dolphins (Tursiops truncatus) found dead following the Deepwater Horizon oil spill*  
PLoS ONE (3.534)

S.Venn-Watson, K. M. Colgrove, **J. Litz (NMFS)**, M. Kinsel, **E. Fougères (NMFS)**, **B. Mase (NMFS)**, K. Terio, J. Saliki, S. Fire, **E. Stratton (NMFS)**, R. Carmichael, D. Odell, D. Shannon, S. Shippee, S. Smith, L. Staggs, M. Tumlin, **R.**



## NOAA SCIENTIFIC PUBLICATIONS REPORT

### JUNE 19, 2015

**Ewing (NMFS), D. Fauquier (NMFS), G. Lovewell, D. Rotstein, W. McFee (NOS/NCCOS/CCEHBR), and T. Rowles (NMFS)**

- This study presents data that supports the hypothesis that contaminants from the Deepwater Horizon (DWH) spill contributed to a bottlenose dolphin unusual mortality event (UME) in Louisiana, Mississippi, and Alabama.
- Results indicate that rare adrenal gland and lung lesions in UME dolphins are consistent with exposure to elevated PAH levels detected in coastal Gulf of Mexico waters during and after the DWH spill.

There has been a northern Gulf of Mexico cetacean unusual mortality event (UME) from February 2010 continuing through 2014, involving primarily bottlenose dolphins (*Tursiops truncatus*) in Louisiana, Mississippi, and Alabama.

Overlapping in time and space with this UME was the Deepwater Horizon (DWH) oil spill, which has been proposed as a contributing cause of moderate to severe lung disease and hypoadrenocorticism in live dolphins examined during 2011 in Barataria Bay, Louisiana. To assess potential contributing factors and causes of deaths for stranded UME dolphins from June 2010 through December 2012, lung and adrenal glands were evaluated from 46 fresh dead carcasses that stranded in Louisiana (including 22 from Barataria Bay), Mississippi, and Alabama. UME dolphins were also evaluated for evidence of biotoxigenesis, morbillivirus infection, and brucellosis. Results were compared to up to 106 fresh dead stranded reference dolphins from outside the UME area or prior to the DWH spill. UME dolphins were more likely to have primary bacterial pneumonia, with 67% dying from this condition. UME dolphins also had thin adrenal cortices compared to reference dolphins. While the overarching cause(s) of and contributors to the longest and largest dolphin Gulf of Mexico UME remains unknown, the otherwise rare adrenal gland and lung lesions identified in live and dead dolphins may be life-threatening health conditions that, in other mammalian models, are consistent with exposure to elevated PAH levels detected in coastal GoM waters during and after the DWH spill.

Expected publication date: June 2015

Available Online:

<http://journals.plos.org/plosone/article?id=10.1371/journal.pone.0126538>



## NOAA SCIENTIFIC PUBLICATIONS REPORT

### JUNE 19, 2015

*Seasonal variation in the skin transcriptome of common bottlenose dolphins*  
(*Tursiops truncatus*) from the northern Gulf of Mexico  
PLoS ONE (3.534)

**F. M. Van Dolah (NOS/NCCOS), M. G. Neely (NOS/NCCOS), L. McGeorge (NOS/NCCOS), B. C. Balmer (NOS/NCCOS), G. M. Ylitalo (NMFS/NWFSC), E. S. Zolman (NOS/NCCOS), T. Speakman (NOS/NCCOS), C. Sinclair (NMFS/SEFSC), N. M. Kellar (NMFS/SWFSC), P. E. Rosel (NMFS/SEFSC), K. L. Mullin (NMFS/SEFSC), and L. H. Schwacke (NOS/NCCOS)**

- The authors investigated the use of skin gene expression profiling to monitor health and contaminant exposure in common bottlenose dolphins (*Tursiops truncatus*).
- Skin gene expression profiling would allow health monitoring with minimal disruption to this protected species.
- Similar to persistent organic pollutant levels in blubber of bottlenose dolphins, the authors found that season had a profound effect on skin gene expression, with nearly one-third of all genes on the array differing significantly in expression levels between winter and the warmer seasons.
- Seasonal effects have not previously been considered in studies assessing gene expression in cetaceans, but clearly must be taken into account when applying transcriptomic analyses to investigate their contaminant exposure or health status.

The use of cetaceans as sentinels to assess environmental impacts of anthropogenic activities requires the establishment of baseline health parameters. As protected species, measurements obtained with minimal disruption to free ranging animals are highly desirable. In this study we investigated the utility of skin gene expression profiling to monitor health and contaminant exposure in common bottlenose dolphins (*Tursiops truncatus*). Remote integument biopsies were collected in the northern Gulf of Mexico prior to the *Deepwater Horizon* oil spill (May 2010) and during summer and winter for two years following oil contamination (2010-2011). A bottlenose dolphin microarray was used to characterize the skin transcriptomes of 94 individuals from three populations: Barataria Bay, Louisiana, Chandeleur Sound, Louisiana, and Mississippi Sound, Mississippi/Alabama. Skin transcriptomes did not differ significantly between populations. In contrast, season had a profound effect on gene expression, with nearly one-third of all genes on the array differing in expression between winter



## NOAA SCIENTIFIC PUBLICATIONS REPORT

### JUNE 19, 2015

and the warmer seasons (moderated T-test;  $p < 0.01$ , fold-change  $> 1.5$ ). Persistent organic pollutants (POPs) in blubber changed concurrently, reaching >two-fold higher concentrations in summer compared to winter, due to a seasonal decrease in blubber thickness and loss of stored lipid. However, global gene expression did not correlate strongly with seasonally changing contaminant concentrations, most likely because the refractory, lipid-stored metabolites are not substrates for phase I or II xenobiotic detoxification pathways. Rather, processes related to cell proliferation, motility, and differentiation dominated the differences in expression in winter and the warmer seasons. More subtle differences were seen between spring and summer (1.5% of genes differentially expressed). However, two presumed oil-exposed animals from spring presented gene expression profiles more similar to the summer animals (presumed exposed) than to other spring animals. Seasonal effects have not previously been considered in studies assessing gene expression in cetaceans, but clearly must be taken into account when applying transcriptomic analyses to investigate their contaminant exposure or health status.

Accepted: 4 June 2015

Expected publication date: Summer 2015

*Photogrammetry of killer whales using a small hexacopter launched at sea*

Journal of Unmanned Vehicle Systems

**J.W. Durban**, (NMFS/SWFSC), **H. Fearnbach** (NMFS/SWFSC), L. G. Barrett-Lennard, W. L. **Perryman** (NMFS/SWFSC), and D. J. LeRoi

- This study was the first application of a UAS system for whale photogrammetry and the first published marine application of a multi-copter for wildlife research.
- Results indicate that the UAS can take high resolution photographs that are sharp enough to differentiate individual free-ranging whales without disturbing them.
- This first application at sea demonstrated the APH-22 hexacopter to be a safe and cost-effective platform for collecting photogrammetry images to fill key scientific data gaps about whales.

Conventional aircraft used for photogrammetry studies of free-ranging whales are often not affordable or practical in remote regions. Researchers report on the use of a small, unmanned hexacopter (APH-22; Aerial Imaging Solutions) as an



## NOAA SCIENTIFIC PUBLICATIONS REPORT

### JUNE 19, 2015

alternative method for collecting photographs to measure killer whales (*Orcinus orca*) at sea. Researchers deployed and retrieved the hexacopter by hand during 60 flights (average duration 13.2 minutes, max = 15.7) from the upper deck of an 8.2m boat, utilizing the aircraft's vertical takeoff and landing (VTOL) capability. The hexacopter was quiet and stable in flight, and therefore could be flown at relatively low altitudes without disturbing whales. The payload was a Micro Four-Thirds system camera that was used to obtain 18,920 still images from an altitude of 35-40m above the whales. Images retrieved were sharp enough to differentiate individual whales using natural markings (77 whales in total) and preliminary estimates resolved differences in whale lengths ranging from 2.6m to 5.8m. This first application at sea demonstrated the APH-22 hexacopter to be a safe and cost-effective platform for collecting photogrammetry images to fill key scientific data gaps about whales, which could be potentially extended to studies of other wildlife species.

Accepted: 26 May 2015

*Spatial and temporal changes in cumulative human impacts on the world's ocean*  
Nature Communications (10.742)

B. S. Halpern, M. Frazier, J. Potapenko, **K. S. Casey (NESDIS/NCEI)**, K. Koenig, C. Longo, J. S. Lowndes, R. C. Rockwood, E. R. Selig, K. A. Selkoe, and S. Walbridge

- Nearly 66% of the ocean and 77% of national jurisdictions show increased human impact compared, driven mostly by climate change pressures.
- Large-scale guidance about where to prioritize management efforts and affirm the importance of addressing climate change to maintain and improve the condition of marine ecosystems are provided.

Human pressures on the ocean are thought to be increasing globally, yet we know little about their patterns of cumulative change, which pressures are most responsible for change, and which places are experiencing the greatest increases. Managers and policymakers require such information to make strategic decisions and monitor progress towards management objectives. Here we calculate and map globally recent change over five years in cumulative impacts to marine ecosystems from fishing, climate change, and ocean- and land-based stressors. Nearly 66% of the ocean and 77% of national jurisdictions show increased human impact, driven mostly by climate change pressures. Five percent of the ocean is heavily impacted with increasing pressures, requiring management attention. Ten percent has very



## NOAA SCIENTIFIC PUBLICATIONS REPORT

### JUNE 19, 2015

low impact with decreasing pressures. Our results provide large-scale guidance about where to prioritize management efforts and affirm the importance of addressing climate change to maintain and improve the condition of marine ecosystems.

Accepted: 21 May 2015

#### ADDITIONAL ARTICLES

##### NWS Publications

*Ensemble Bayesian forecasting system Part I: theory and algorithms*

Journal of Hydrology (2.693)

**H. Herr (NWS/NWC) and R. Krzysztofowicz**

- The algorithm provides another option for implementing a hydrologic ensemble forecasting system.
- These techniques can be used in conjunction to generate an ensemble forecast that accounts for total uncertainty about the future predictand.

The ensemble Bayesian forecasting system (EBFS), whose theory was published in 2001, is developed for the purpose of quantifying the total uncertainty about a discrete-time, continuous-state, non-stationary stochastic process such as a time series of stages, discharges, or volumes at a river gauge. The EBFS is built of three components: an input ensemble forecaster (IEF), which simulates the uncertainty associated with random inputs; a deterministic hydrologic model (of any complexity), which simulates physical processes within a river basin; and a hydrologic uncertainty processor (HUP), which simulates the hydrologic uncertainty (an aggregate of all uncertainties except input). It works as a Monte Carlo simulator: an ensemble of time series of inputs (e.g., precipitation amounts) generated by the IEF is transformed deterministically through a hydrologic model into an ensemble of time series of outputs, which is next transformed stochastically by the HUP into an ensemble of time series of predictands (e.g., river stages).

Previous research indicated that in order to attain an acceptable sampling error, the ensemble size must be on the order of hundreds (for probabilistic river stage forecasts and probabilistic flood forecasts) or even thousands (for probabilistic stage transition forecasts). The computing time needed to run the hydrologic model this many times renders the straightforward simulations operationally infeasible.

This motivates the development of the ensemble Bayesian forecasting system with randomization (EBFSR), which takes full advantage of the analytic meta-Gaussian



## NOAA SCIENTIFIC PUBLICATIONS REPORT

### JUNE 19, 2015

HUP and generates multiple ensemble members after each run of the hydrologic model; this auxiliary randomization reduces the required size of the meteorological input ensemble and makes it operationally feasible to generate a Bayesian ensemble forecast of large size. Such a forecast quantifies the total uncertainty, is well calibrated against the prior (climatic) distribution, possesses a Bayesian coherence property, constitutes a random sample of the predictand, and has an acceptable sampling error — which makes it suitable for rational decision making under uncertainty.

Published: May 2015

Available Online:

<http://www.sciencedirect.com/science/article/pii/S0022169414009949>

*Hydroclimatic Conditions Preceding the March 2014 Oso Landslide*

Journal of Hydrometeorology (3.57)

B. Henn, Q. Cao, D. P. Lettenmaier, C. S. Magirl, C. Mass, **J. B. Bower**, **M. St. Laurent**, Y. Mao, and **S. Perica (NOAA/NWS)**

- While the precipitation observed leading up to the 2014 Oso landslide was heavy, the 21–42-day precipitation accumulations would be expected to occur as often as every 3 yr, or no more rarely than every 5–6 yr.
- This heavy precipitation occurred in the context of a 4-yr period of above-average precipitation.
- The period of high precipitation in the weeks before the landslide came near the end of the seasonal wet period, when soil moisture was already high.

The 22 March 2014 Oso landslide was one of the deadliest in U.S. history, resulting in 43 fatalities and the destruction of more than 40 structures. The authors examined the synoptic conditions, precipitation records, and soil moisture reconstructions in the days, months, and years preceding the landslide.

Atmospheric reanalysis showed a period of enhanced moisture transport to the Pacific Northwest beginning on 11 February 2014. The 21–42-day periods prior to the landslide had anomalously high precipitation; approximately 300–400 mm of precipitation fell at Oso in the 21 days prior to the landslide. Relative only to historical periods ending on 22 March, the return periods of these precipitation accumulations are large (25–88 yr), however, relative to the largest accumulations from any time of the year (annual maxima), return periods are more modest (2–6 yr). In addition to the 21–42 days prior to the landslide, there is a secondary



## NOAA SCIENTIFIC PUBLICATIONS REPORT

### JUNE 19, 2015

maximum in the precipitation return periods for the 4 yr preceding the landslide. Reconstructed soil moisture was also anomalously high prior to the landslide. By placing hydroclimatic conditions during the event in historical context, our analysis should contribute to a better understanding of the events leading to the landslide. Expected publication date: March 2015

#### NESDIS Publications

*Data stewardship: how NOAA delivers environmental information for today and tomorrow*

Marine Technology Society Journal (0.76)

**J. Cartwright, S. McLean, and J. Varner (NESDIS/NCEI)**

- NCEI provides easy, open access to public data via long-term archiving and stewardship.
- This is accomplished through a geospatial framework that is versatile, robust, and extensible.
- The basis of this framework is a sustainable suite of data services built on spatially enabled databases, standard-based Web services, and ISO metadata.

National Oceanic and Atmospheric Administration's (NOAA's) National Geophysical Data Center (NGDC) ensures the security and widespread availability of scientific marine geophysical data through long-term stewardship. Marine geophysical data extend from the water surface, through the water column, to the seafloor and even the geology beneath. In addition to ensuring the quality, integrity, and accessibility of these data, NGDC develops derived products such as precise representations of Earth's magnetic field and digital elevation models for coastal and marine areas. NOAA and our partners expend significant resources to survey our coasts and oceans. In order to maximize the return on this investment, the data must be easily discoverable and readily accessible by numerous users and applications now and well into the future. To meet these goals, NGDC is drawing on a variety of software technologies and is strictly adhering to international data standards. The result is a geospatial framework built on spatially enabled databases, standard-based Web services, and International Standards Organization (ISO) metadata. NGDC's suite of tools and services delivers over 40 TB of marine geophysical data each year to a wide range of customers. By making the data more accessible to both human and machine clients, NGDC extends the use of, and



## NOAA SCIENTIFIC PUBLICATIONS REPORT

### JUNE 19, 2015

therefore the value of, these data. The result is environmental information that enables informed decisions.

Accepted: 31 March 2015

#### *A metadata template for ocean acidification data*

Earth System Science Data (ALM: 176 downloads since 11 June 2015)

L. Q. Jiang, S. O'Connor, **K. M. Arzayus** and **A. R. Parsons**

**(NOAA/NESDIS/National Centers for Environmental Information)**

- This paper describes a first ever metadata template that can be used to document biological experimental data, as well as other commonly seen ocean acidification (OA) data sets.
- A standard OA template clears one of the major roadblocks for effective data management.
- The authors described a metadata template that applies to many types of OA data sets, including chemical OA data sets and those describing biological responses to OA.
- In addition to serving OA data management efforts, the template can be used by the OA research community for documenting their OA data, sharing data among researchers, and submitting data to data centers.

This paper defines the best practices for documenting ocean acidification (OA) data and presents a framework for an OA metadata template. Metadata is structured information that describes and locates an information resource. It is the key to ensuring that a data set will be accessible into the future. With the rapid expansion of studies on biological responses to OA, the lack of a common metadata template to document the resulting data poses a significant hindrance to effective OA data management efforts. In this paper, we present a metadata template that can be applied to a broad spectrum of OA studies, including those studying the biological responses to OA. The “variable metadata section”, which includes the variable name, observation type, whether the variable is a manipulation condition or response variable, and the biological subject on which the variable is studied, forms the core of this metadata template. Additional metadata elements, such as investigators, temporal and spatial coverage, and data citation are essential components to complete the template. We explain the structure of the template, and define many metadata elements that may be unfamiliar to researchers.



## NOAA SCIENTIFIC PUBLICATIONS REPORT

### JUNE 19, 2015

Accepted: 18 May 2015

Available Online: <http://www.earth-syst-sci-data-discuss.net/8/1/2015/essdd-8-1-2015.html>

#### NMFS Publications

*Mixed stock analysis of a resident green turtle, *Chelonia mydas*, population in New Caledonia links rookeries in the South Pacific*

Wildlife Research (1.194)

T. C. Read, N. N. FitzSimmons, L. Wantiez, **M. P. Jensen (NMFS/SWFSC)**, F. Keller, O. Chateau, R. Farman, J. Werry, K. T. MacKay, G. Petro and C. J. Limpus

- This study examines the genetic diversity of green turtle populations, finding that rookeries in the d'Entrecasteaux Islands, New Caledonia, and Vanuatu form unique genetic stocks and that the Chesterfield Islands rookeries are linked to the Coral Sea genetic stock.
- The mixed stock analysis indicates the highest proportion (mean = 0.63) of foraging green turtles originate from d'Entrecasteaux stock.
- Marine conservation policies in New Caledonia need to consider the links between the foraging and nesting populations of *C. mydas* in New Caledonia to other rookeries and foraging grounds in the Coral Sea.

Migratory species pose a challenge for conservation. Their complex life history makes it difficult to implement efficient conservation actions. In New Caledonia, large seagrass habitats in the Grand Lagon Sud (GLS) are home to resident green turtles (*Chelonia mydas*) of unknown origins. To assess the stock composition in the GLS, 164 foraging turtles were sampled for genetic analysis of ~770 bp of the mitochondrial (mt)DNA control region at five different sites between September 2012 and December 2013. To provide baseline data for mixed stock analysis, published data from rookeries were used in addition to 105 samples collected at rookeries in the d'Entrecasteaux Islands and Chesterfields Islands in New Caledonia and at Malekula Island in Vanuatu. Exact tests of population differentiation and pairwise  $F_{ST}$  estimates were used to test for differences in mtDNA haplotype frequencies. These analyses indicated that rookeries in the d'Entrecasteaux Islands and Vanuatu form unique genetic stocks and that the Chesterfield Islands rookeries are linked to the Coral Sea genetic stock. Mixed stock analysis indicated the highest proportion (mean = 0.63) of foraging turtles originate from d'Entrecasteaux stock. Marine conservation policies for green turtles needs to consider the links between the foraging and nesting populations of



## NOAA SCIENTIFIC PUBLICATIONS REPORT

### JUNE 19, 2015

*C. mydas* in New Caledonia to other rookeries and foraging grounds in the Coral Sea.

Accepted: 17 May 2015

*Variation in phytoplankton composition between two North Pacific frontal zones along 158°W during winter-spring 2008-2011*

Progress in Oceanography (3.986)

E. Howell, **S. Bograd** (NMFS/SWFSC), A. Hoover, M. Seki, and J. Polovina

- This paper examines the lower trophic community composition at two basin-scale frontal regions of the North Pacific Transition Zone, which are important foraging and migration corridors for a number of top predator species.
- Results show that phytoplankton class composition was consistent at each front through time, but significantly different between fronts.
- Continued in situ and remote monitoring will provide important baseline information about the phytoplankton composition in this important ecological zone.

Data from three research cruises along the 158°W meridian through the North Pacific Subtropical Frontal Zone (STF) during spring 2008, 2009 and 2011 were used to estimate phytoplankton functional types and size classes. These groups were used to describe phytoplankton composition at the North Pacific Subtropical (STF) and Transition Zone Chlorophyll (TZCF) Fronts, which represent ecologically important large-scale features in the central North Pacific.

Phytoplankton class composition was consistent at each front through time, yet significantly different between fronts. The STF contained lower integrated chlorophyll-a concentrations, with surface waters dominated by picophytoplankton and a deep chlorophyll maximum equally comprised of pico- and nanophytoplankton. The TZCF contained significantly higher concentrations of nanophytoplankton through the water column, specifically the prymnesiophyte group. Integrated chlorophyll-a concentrations at the TZCF were 30-90% higher than at the STF, with the dominant increase in the signal from the nanophytoplanktonic prymnesiophyte group. The meridional position of the STF was consistently located near 32°N through these three years, with the more spatially variable TZCF ranging from 2°-4° further north of the STF. This variability in the frontal position of the TZCF may lead to ecological impacts



## NOAA SCIENTIFIC PUBLICATIONS REPORT

### JUNE 19, 2015

though the food web. Continued in-situ and remote monitoring, specifically during El Niño and ENSO neutral phases, will provide additional ecological information to help understand mechanistic causes of phytoplankton variability in this important ecological region.

Expected Publication date: 1 September 2015

*Using a remotely operated vehicle (ROV) to observe loggerhead sea turtle (Caretta caretta) behavior on foraging grounds off the mid-Atlantic United States*

Journal of Experimental Marine Biology and Ecology (2.475)

R. J. Smolowitz, S. H. Patel, **H. L. Haas**, and S. Miller (NMFS/NEFSC)

- Demonstrates a new, safer way to observe turtle behavior
- Documents cold water, benthic feeding in the Mid-Atlantic.
- A brief compilation of the footage from these surveys can be found at:  
<http://coonamessettfarmfoundation.org/media/videos/>

This study represents the first documented use of a remotely operated vehicle (ROV) to actively track sea turtles in situ. From 2008 to 2014, an ROV was deployed to track the at-sea behavior of loggerhead turtles in the Northwest Atlantic Ocean. Seventy turtles were tracked, totaling 44.7 h of direct turtle footage. For all attempts, usable video with a turtle retained in view for a minimum of 30 s, was produced at a rate of 43.5% of effort. Turtles were first spotted from the boat, and then when the turtle was within ~ 50 m of the boat, the ROV was deployed to track the turtle for as long as possible. Tracking durations reached up to 426.1 min. Tracked turtles often remained within ~ 10 m of the surface; however loggerheads were tracked to the seafloor on 12 occasions. Turtles were filmed foraging both pelagically and benthically, even though bottom temperatures reached as low as 7.1 °C. A range of inter- and intra-species interactions were also captured. Several varieties of fish remained associated with individual turtles for extended periods of time, even during benthic foraging dives. Additionally, a variety of social interactions between loggerheads were documented. Generally these interactions were filmed occurring near the ocean surface. Overall, using the ROV provided great insight into loggerhead at-sea behavior, otherwise unattainable using previously established techniques.

Expected publication date: 3 June 2015

Available Online:

<http://www.sciencedirect.com/science/article/pii/S0022098115001343>



## NOAA SCIENTIFIC PUBLICATIONS REPORT

### JUNE 19, 2015

*Stable isotope models predict foraging habitat of Northern Fur Seals (*Callorhinus ursinus*) in Alaska*

PLoS ONE (3.534)

**T. K. Zeppelin, D. S. Johnson, C. E. Kuhn, S. J. Iverson, and R. R. Ream**  
(NMFS/AKFSC)

- Describes the development of an innovative model which uses stable isotopes from blood to predict foraging habitat of northern fur seals.
- Constructing predictive models using stable isotopes provides an effective means to assess habitat use at the population level, is inexpensive, and can be applied to other marine predators

We developed models to predict foraging habitat of adult female northern fur seals (*Callorhinus ursinus*) using stable carbon ( $\delta^{13}\text{C}$ ) and nitrogen ( $\delta^{15}\text{N}$ ) isotope values from plasma and red blood cells. Binomial generalized linear mixed models were developed using blood isotope samples collected from 35 adult female fur seals on three breeding colonies in Alaska during July-October 2006. Satellite location and dive data were used to define habitat use in terms of the proportion of time spent or dives made in different oceanographic/bathymetric domains. For both plasma and red blood cells, the models accurately predicted habitat use for animals that foraged exclusively off or on the continental shelf. The models did not perform as well in predicting habitat use for animals that foraged in both on- and off-shelf habitat; however, sample sizes for these animals were small. Concurrently collected scat, fatty acid, and dive data confirmed that the foraging differences predicted by isotopes were associated with diet differences. Stable isotope samples, dive data, and GPS location data collected from an additional 15 females during August-October 2008 validated the effective use of the models across years. Little within year variation in habitat use was indicated from the comparison between stable isotope values from plasma (representing 1-2 weeks) and red blood cells (representing the prior few months). Constructing predictive models using stable isotopes provides an effective means to assess habitat use at the population level, is inexpensive, and can be applied to other marine predators.

Published: 1 June 2015

Available Online:

<http://Journals.plos.org/plosone/article?id=10.1371/Journal.pone.0127615>



## NOAA SCIENTIFIC PUBLICATIONS REPORT

### JUNE 19, 2015

*The ability of blue crab (Callinectes sapidus, Rathbun 1886) to sustain aerobic metabolism during hypoxia*

Journal of Experimental Marine Biology and Ecology (2.475)

**R. W. Brill (NMFS/NEFSC), P. G. Bushnell, T. A. Elton, and H. J. Small**

- Blue crab are tolerant of hypoxia, are oxygen regulators, and at minimal metabolic rates can maintain aerobic metabolism down to ~20 % air saturation.
- Critical oxygen levels are positively correlated with metabolic rate.
- Critical oxygen levels are ~45% air saturation at the highest metabolic rates.

To assess the ability of adult blue crab (*Callinectes sapidus*) to function under the hypoxic conditions becoming increasingly common in their inshore habitats, critical oxygen levels (i.e., the minimum oxygen levels at which aerobic metabolism can be maintained) were determined over a range of metabolic rates using automated intermittent-flow respirometry. Different metabolic rates were induced by conducting experiments at three temperatures (17°, 23°, and 28°C), testing recently fed crabs, and those infected with the parasitic dinoflagellate *Hematodinium perezii*. The effects of hypoxia on the metabolic rates and recovery times of individuals following enforced exhaustive activity, and metabolic rates following feeding, were also measured to determine the levels of hypoxia likely to impact feeding, digestion, and overall energetics. Contrary to previously published results, blue crab were found not to be partial oxygen conformers (i.e., where metabolic rate falls in concert with reductions in ambient oxygen), but rather to be oxygen regulators (i.e., to have the ability to maintain a constant aerobic metabolic rate until the critical oxygen level was reached). By this measure, at routine metabolic rates blue crab are as hypoxia-tolerant as other decapod crustaceans with a median critical oxygen level of ~20% air saturation (at 17° and 23°C). Critical oxygen levels increased in concert with the increases in metabolic rate occurring at 28°C, in individuals infected with *Hematodinium perezii*, and those recently fed. At the highest metabolic rates (measured in recently fed individuals at 28°C) median critical oxygen level was ~45% air saturation. Consistent with this latter observation, metabolic rates after feeding or exercise were not compromised until below 50% air saturation, although maximum metabolic rates were lower at this level of hypoxia. The results presented are consistent with the oxygen levels shown to influence crab behaviors (~2 to 4 mg l<sup>-1</sup>) in both field and laboratory settings.

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*Stock composition and ocean spatial distribution inference from California recreational Chinook salmon fisheries using Genetic Stock Identification*  
Fisheries Research (1.843)

**W. H. Satterthwaite**, J. Ciancio, E. Crandall, M. L. Palmer-Zwahlen, A. M. Grover, **M. R. O'Farrell**, **E. C. Anderson**, **M. S. Mohr**, and **J. C. Garza**  
(NFMS/SWFSC)

- We describe methods of accounting for sampling, process, and assignment errors in estimating stock-specific catch and catch composition.
- Genetic stock identification quantified harvest of tagged and untagged salmon stocks.
- Spatial patterns for untagged stocks were similar to tagged management proxies.

We apply genetic stock identification (GSI) data and models of the catch and sampling process to describe spatial and temporal patterns in the stock composition and stock-specific catch-per-unit-effort (CPUE) of both tagged and untagged stocks encountered in California recreational ocean Chinook salmon fisheries during the period 1998-2002. Spatial and temporal distributions inferred from GSI sampling of stocks with tagged hatchery components were broadly consistent with those previously inferred from studies of tag recoveries alone, while GSI provided additional insight into untagged stocks of conservation concern. The catch in all times and areas was dominated (typically  $\geq 90\%$ ) by the "Central Valley Fall" genetic reporting group, which is comprised primarily of Sacramento River fall run Chinook. Other contributing stocks were more spread out in space and time with the exception of Central Valley winter run Chinook, which were rarely encountered by boats fishing in port areas north of Point Reyes. Localized



## NOAA SCIENTIFIC PUBLICATIONS REPORT

### JUNE 19, 2015

stock-specific CPUE appeared to increase near a stock's respective natal river while decreasing in other port areas at the time of adult return to freshwater for spawning. We describe methods for quantifying uncertainty in stock proportions, stock-specific catch, and determining the statistical support for proposed management boundaries hypothesized to represent "break points" in the spatial distributions for stocks of concern, and find at most equivocal support for a proposed delineation line at Point Reyes in north-central California.

Accepted: 1 June 2015

*Geostatistical delta-generalized linear mixed models improve precision for estimated abundance indices for West Coast groundfishes*

ICES Journal of Marine Science (2.525)

**J. T. Thorson, A. O Shelton, E. J. Ward, and H. Skaug (NMFS/NWFSC)**

- This paper demonstrates a computationally efficient implementation of spatial models for estimating abundance indices.
- Abundance indices are commonly used in stock assessments through the U.S. and worldwide, and this paper demonstrates substantial improves in estimation using simulated data and 28 case-study species.

Indices of abundance are the bedrock for stock assessments or empirical management procedures used to manage fishery catches for fish populations worldwide, and are generally obtained by processing catch-rate data. Recent research suggests that geostatistical models can explain a substantial portion of variability in catch rates via the location of samples (i.e. whether located in high- or low-density habitats), and thus use available catch-rate data more efficiently than conventional "design-based" or stratified estimators. However, the generality of this conclusion is currently unknown because geostatistical models are computationally challenging to simulation-test and have not previously been evaluated using multiple species. We develop a new maximum likelihood estimator for geostatistical index standardization, which uses recent improvements in estimation for Gaussian random fields. We apply the model to data for 28 groundfish species off the U.S. West Coast and compare results to a previous



## NOAA SCIENTIFIC PUBLICATIONS REPORT

### JUNE 19, 2015

“stratified” index standardization model, which accounts for spatial variation using post-stratification of available data. This demonstrates that the stratified model generates a relative index with 60% larger estimation intervals than the geostatistical model. We also apply both models to simulated data and demonstrate (i) that the geostatistical model has well-calibrated confidence intervals (they include the true value at approximately the nominal rate), (ii) that neither model on average under- or overestimates changes in abundance, and (iii) that the geostatistical model has on average 20% lower estimation errors than a stratified model. We therefore conclude that the geostatistical model uses survey data more efficiently than the stratified model, and therefore provides a more cost-efficient treatment for historical and ongoing fish sampling data.

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Available Online:

<http://icesjms.oxfordJournals.org/content/72/5/1297.abstract?etoc>

*A comparison of single and multiple stressor protocols to assess acute stress in a coastal shark species, Rhizoprionodon terraenovae*

Fish Physiology and Biochemistry (1.68)

**E. R. Hoffmayer, J. M. Hendon, G. R. Parsons, W. B. Driggers III, and M. D. Campbell (NMFS)**

- The stress protocol used to challenge a shark is just as important to consider as the resulting parameter values used to evaluating the responses.
- This study showed that the serial sample protocol is ideal for studies investigating changes inherent to individuals, while the single sample protocol is more appropriate for population level analyses.

Elasmobranch stress responses are traditionally measured in the field by either singly or serially sampling an animal after a physiologically stressful event. Although capture and handling techniques are effective at inducing a stress response, differences in protocols could affect the degree of stress experienced by an individual, making meaningful comparisons between the protocols difficult if not impossible. In this study, the authors acutely stressed Atlantic sharpnose sharks, *Rhizoprionodon terraenovae*, by standardized capture (rod and reel) and handling methods and implemented either a single or serial blood sampling protocol to monitor four indicators of the secondary stress response. Singly sampled sharks were hooked and allowed to swim around the boat until retrieved for a blood sample at either 0, 15, 30, 45, or 60 minutes post hooking. Serially



## NOAA SCIENTIFIC PUBLICATIONS REPORT

### JUNE 19, 2015

sampld sharks were retrieved, phlebotomized, released while still hooked, and subsequently resampled at 15, 30, 45, and 60 minutes post hooking. Blood was analyzed for hematocrit, and plasma glucose, lactate, and osmolality levels. Although both single and serial sampling protocols resulted in an increase in glucose, no significant difference in glucose level was found between protocols. Serially sampled sharks exhibited cumulatively heightened levels for lactate and osmolality at all time intervals as compared to single sampled animals at the same time. Maximal concentration differences of 217.5%, 9.8%, and 41.6% were reported for lactate, osmolality, and glucose levels, respectively. Hematocrit increased significantly over time for the single sampling protocol, but did not change significantly during the serial sampling protocol. The differences in resultant blood chemistry levels between implemented stress protocols and durations are significant and need to be considered when assessing stress in elasmobranchs.

Accepted: 26 May 2015

*Age at maturity, skipped spawning, fecundity, and site fidelity of female sablefish (Anoplopoma fimbria) during the spawning season*

Fishery Bulletin (1.783)

**C. J. Rodgveller, J. W. Stark, K. B. Echave, and P. J. F. Hulson**  
(NMFS/AKFSC)

- Skipped spawning was documented for the first time in female sablefish, and may vary with environmental conditions.
- Updated maturity at age data is now available for stock assessment of sablefish.

Accurate maturity at age data is necessary for estimating spawning stock biomass and setting fishing reference points. This is the first age at maturity study of female sablefish sampled in Alaska near their winter spawning period when maturity is most easily assessed. Skipped spawning in female sablefish, fish that have spawned in the past but are not in the current season, were documented for the first time. Age at maturity was heavily influenced by whether these skipped spawners were classified as mature or immature; the age at 50% maturity when skipped spawners were classified as mature was 6.8 years and 9.9 when classified as immature. Skipped spawning was more common in some areas and rates of skipped spawning were higher for older females. Winter estimates of age at



## NOAA SCIENTIFIC PUBLICATIONS REPORT

### JUNE 19, 2015

maturity were more similar to estimates collected in the summer when skipped spawners were classified as mature in the winter (skipped spawning was not identified in the summer). When skipped spawners were considered immature during the winter, estimates of spawning biomass decreased substantially. Relative fecundity did not change with size and age, verifying the assumption made in the Alaska sablefish stock assessment that relative reproductive output is linearly related to female spawning biomass. Four female sablefish were satellite tagged during the spawning season. Although sablefish are highly migratory throughout their lives, the limited results indicate that sablefish have site fidelity during the spawning season.

Accepted: 12 March 2015

*Mixed effects: a unifying framework for statistical modelling in fisheries biology*  
ICES Journal of Marine Science (2.525)

**J. T. Thorson (NMFS/NWFSC), and C Minto**

- This paper serves as a concise but complete introduction to mixed-effects modelling, a recently developed statistical framework that generalizes many classic fisheries models.
- The authors present examples and working code for many different applications, including spatial, genetics, and individual growth models.

Fisheries biology encompasses a tremendous diversity of research questions, methods, and models. Many sub-fields use observational or experimental data to make inference about biological characteristics that are not directly observed (called “latent states”), such as heritability of phenotypic traits, habitat suitability, and population densities to name a few. Latent states will generally cause model residuals to be correlated, violating the assumption of statistical independence made in many statistical modelling approaches. In this article, the authors argue that mixed-effect modelling (i) is an important and generic solution to non-independence caused by latent states; (ii) provides a unifying framework for disparate statistical methods such as time-series, spatial, and individual-based models; and (iii) is increasingly practical to implement and customize for problem-specific models. They offer a summary of the distinctions between *fixed* and *random* effects, review a generic approach for parameter estimation, and distinguish general categories of non-linear mixed-effect models. Finally, the authors provide four worked examples, including state-space, spatial, individual-



## NOAA SCIENTIFIC PUBLICATIONS REPORT

### JUNE 19, 2015

level variability, and quantitative genetics applications (with working code for each), while providing comparison with conventional fixed-effect implementations, and conclude by summarizing directions for future research in this important framework for modelling and statistical analysis in fisheries biology.

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<http://icesjms.oxfordJournals.org/content/72/5/1245.abstract?etoc>

*Genetic origins of immature green turtles (Chelonia mydas) at two foraging grounds in Sabah, Malaysia*

Endangered Species Research (2.259)

**M. P. Jensen (NMFS/SWFSC), N. Pilcher, and N. N. FitzSimmons**

- Mixed Stock Analysis (MSA) was used to trace the origin of 90 immature green turtles sampled at two foraging grounds, Mantanani Island and Layang Layang Island, located off the coast of northwest Sabah, Malaysia.
- The majority of the turtles foraging at Mantanani originated from three important populations in Southeast Asia located up to 1500 km away (Turtle Islands of Sarawak, Malaysia and Philippine Turtle Islands and Peninsular Malaysia).
- These rookeries have a tradition of using unshaded beach hatcheries that have resulted in mostly female hatchlings. This may have contributed to the observed 1:4 female bias of turtles at the foraging grounds.
- The paper discuss the implications of hatchery practices at nesting beaches and recommend future research to improve the management of marine turtles where hatcheries are commonly used.

Understanding population dynamics in both breeding and foraging habitats is a vital part of assessing the long-term viability of any species, particularly those that are highly migratory, such as the green turtle *Chelonia mydas*. Monitoring of marine turtle populations at foraging grounds may help detect early signs of population trends that would otherwise take decades to be seen at nesting beaches. Mixed Stock Analysis (MSA) using molecular marker techniques provides an effective tool for estimating the origin of turtles sampled at foraging grounds or along migratory routes. Here we use sequence data from the mitochondrial DNA (mtDNA) control region of 90 immature green turtles at two foraging grounds at Mantanani Island and Layang Layang Island located off the coast of northwest



## NOAA SCIENTIFIC PUBLICATIONS REPORT

### JUNE 19, 2015

Sabah, Malaysia. We used data from 30 Indo-Pacific green turtle populations as the baseline for tracing back the origin of turtles sampled at the two foraging grounds. The origins of the foraging turtles at the two locations were not different and the majority of the turtles originated from three important populations in Southeast Asia located up to 1500 km away. These included the Turtle Islands of Sarawak in north-western Borneo (mean contribution = 30%), the Malaysia and Philippine Turtle Islands off SE Sabah (mean = 28%) and Peninsular Malaysia (mean = 31%). These rookeries have a long tradition of using unshaded beach hatcheries that have resulted in mostly female hatchlings, which may have contributed to the observed 1:4 female bias of turtles at the foraging grounds. We discuss the implications of hatchery practices at nesting beaches and recommend future research to improve the management of marine turtles where hatcheries are commonly used.

Accepted: 11 May 2015

#### *Productivity change and fleet restructuring after transition to individual transferable quota management*

Marine Policy (2.621)

R. Färe, S. Grosskopf, and **J. Walden (NOAA/NEFSC)**

- This study constructs the Färe-Primont index to measure productivity change for the Mid-Atlantic surf clam and ocean quahog fishery over a 32 year time period, including time periods before and after the transition to an individual transferable quota (ITQ) management system of fishery vessels.
- Aggregate productivity change post-ITQ is driven by continuing vessels.

Productivity change in fisheries after transition to an individual transferable quota (ITQ) management system is driven by exit of some vessels, entry of other vessels, and changes in productivity of existing vessels. Generally, it is thought that an ITQ system boosts productivity due to the exit of less productive vessels. However, ITQ management systems also create an additional barrier to entry, and more productive vessels may not be able to enter the fishery. This study constructs the Färe-Primont index to measure productivity change for the Mid-Atlantic surf clam and ocean quahog fishery over a 32 year time period, which includes both pre and post-ITQ time periods. The index is then combined with a biomass change index to arrive at a measure of biomass adjusted productivity change. Results show that when biomass changes are considered, positive productivity gains occurred



## NOAA SCIENTIFIC PUBLICATIONS REPORT

### JUNE 19, 2015

throughout the time period. Further examination of contributions from entering and survivor vessels show that entering vessels had little impact on aggregate productivity, but on an individual basis, they eventually were equal in productivity to survivor vessels.

Accepted: 26 May 2015

#### Joint Line Office Publications

*Synthesis of Arctic Research (SOAR) in marine ecosystems of the Pacific Arctic*  
Progress in Oceanography (3.986)

**S. E. Moore (NMFS/OST) and P. J. Stabeno (OAR/PMEL)**

- This article is a preface to a Special Issue to explore and integrate information from marine research in the Pacific Arctic.

Over the decade 2004-2013 dramatic environmental changes in the Pacific Arctic suggest a 'new normal' climate is emerging. Describing the biophysical properties of the 'new' Pacific Arctic marine ecosystem was foundational to the SOAR effort. Examining biological responses to the new biophysical forcing has focused on the study of lower trophic level communities and upper trophic level species.

Significant conclusions are 1) variable advection and hydrographic processes are key influences on benthic hotspots for seabird and marine mammal predators, 2) six bowhead whale core-use areas are identified, and body condition suggests bowheads are faring well despite sea ice loss, and 3) the Arctic Marine Pulses (AMP) conceptual model aims to animate advection models and link to pelagic-benthic coupling models.

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Available Online:

<http://www.sciencedirect.com/science/article/pii/S0079661115001147>

*NOAA's Role in Defining the U.S. Extended Continental Shelf*  
Marine Technology Society Journal (0.678)

**B. W. Eakins (NESDIS/NCEI), M. L. Bohan (OAR/OER), A. A. Armstrong, M. Westington (NOS), J. Jencks, E. Lim, S. J. McLean, and R. R. Warnken (NESDIS/NCEI)**

- The U.S. Expanded Continental Shelf (ECS) Project has seen significant benefits from marine technological advances, and has contributed to expanded and enhanced metadata standards.



## **NOAA SCIENTIFIC PUBLICATIONS REPORT**

### **JUNE 19, 2015**

- Additional benefits of these data extend beyond the clear establishment of the U.S. ECS.
- Open access to and re-use of these technologies and data will help spur new science and exploration, improve understanding of and management of our ocean resources, and likely impact us in unexpected ways for years to come.

The legal continental shelf is a maritime zone that typically goes out to 200 nautical miles from shore. It may, however, be extended beyond 200 nautical miles, based in part on the morphology of the continental margin. The United Nations Convention on the Law of the Sea sets forth the requirements for how coastal countries can legally define such an extended continental shelf (ECS), within which they may manage the natural resources on and below the seabed. The National Oceanic and Atmospheric Administration (NOAA), along with the U.S. Geological Survey and the U.S. Department of State, is working to map, analyze, and define the seaward extent of the U.S. ECS. New advances in maritime technologies, such as improved multibeam echosounders, and associated visualization and analysis software, aid in this effort by enabling project scientists to better understand seafloor geomorphology, and interpret local and regional geologic processes. Marine geophysical data collected during this project are publicly available, benefiting the broader scientific community and public through timely data access and long-term preservation. To date, NOAA has led more than 30 high-resolution surveys and mapped more than two million square kilometers of sea floor in support of the U.S. ECS effort. New discoveries have been made during these surveys, and the data have contributed to better understanding of the morphology and geology of the U.S. continental margins.

Expected publication date: May 2015